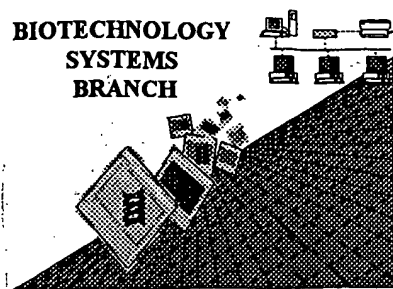


5040 #3  
CW

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/018,445  
Source: Per 110  
Date Processed by STIC: 1/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**  
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)

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U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

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PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002

TIME: 07:44:23

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

114-5

4 <110> APPLICANT: C. Frank Bennett  
 5 Brett P. Monia  
 6 Lex M. Cowser  
 7 ISIS PHARMACEUTICALS, INC.  
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 3 EXPRESSION  
 11 <130> FILE REFERENCE: RTSP-0047  
 13 <140> CURRENT APPLICATION NUMBER: US/10/018,445  
 13 <141> CURRENT FILING DATE: 2001-12-13  
 13 <150> PRIOR APPLICATION NUMBER: US 09/344,520  
 14 <151> PRIOR FILING DATE: 1999-06-25  
 16 <160> NUMBER OF SEQ ID NOS: 47  
 18 <210> SEQ ID NO: 1  
 19 <211> LENGTH: 3170  
 20 <212> TYPE: DNA  
 21 <213> ORGANISM: Homo sapiens  
 23 <220> FEATURE:  
 24 <221> NAME/KEY: CDS  
 25 <222> LOCATION: (21)..(2387)  
 27 <400> SEQUENCE: 1

Does Not Comply  
 Corrected Diskette Needed

28 cgccgcggga ggcggacgag atg cga gcg cgg ccg cgg ccc cgg ccg ctc 50  
 29 Met Arg Ala Arg Pro Arg Pro Arg Leu  
 30 1 5 10  
 32 tgg gtg act gtg ctg gcg ctg ggg gcg ctg ggc ggt ggc gta gga 98  
 33 Trp Val Thr Val Leu Ala Leu Gly Ala Leu Ala Gly Val Gly Val Gly  
 34 15 20 25  
 36 ggg ccc aac atc tgt acc acg cga ggt gtg agc tcc tgc cag cag tgc 146  
 37 Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys Gln Gln Cys  
 38 30 35 40  
 40 ctg gct gtg agc ccc atg tgt gcc tgg tgc tct gat gag gcc ctg cct 194  
 41 Leu Ala Val Ser Pro Met Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro  
 42 45 50 55  
 44 ctg ggc tca cct cgc tgt gac ctg aag gag aat ctg ctg aag gat aac 242  
 45 Leu Gly Ser Pro Arg Cys Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn  
 46 60 65 70  
 48 tgt gcc cca gaa tcc atc gag ttc cca gtg agt gag gcc cga gta cta 290  
 49 Cys Ala Pro Glu Ser Ile Glu Phe Pro Val Ser Glu Ala Arg Val Leu  
 50 75 80 85 90  
 52 gag gac agg ccc ctc agc gac aag ggc tct gga gac agc tcc cag gtc 338  
 53 Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser Gln Val  
 54 95 100 105  
 56 act caa gtc agt ccc cag agg att gca ctc cgg ctc cgg cca gat gat 386  
 57 Thr Gln Val Ser Pro Gln Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp  
 W--> 58 110-110 115-115 120-120 ← fix amino acid numbering  
 60 tcg aag aat ttc tcc atc caa gtg cgg cag gtg gag gat tac cct gtg 434  
 61 Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val  
 62 125 130 135  
 64 gac atc tac tac ttg atg gac ctg tct tac tcc atg aag gat gat ctg 482

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002

TIME: 07:44:23

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

65	Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu	
66	140 145 150	
68	tgg agc atc cag aac ctg ggt acc aag ctg gcc acc cag atg cga aag	530
69	Trp Ser Ile Gln Asn Leu Gly Thr Lys Leu Ala Thr Gln Met Arg Lys	
70	155 160 165 170	
72	ctc acc agt aac ctg cgg att ggc ttc ggg gca ttt gtg gac aag cct	578
73	Leu Thr Ser Asn Leu Arg Ile Gly Phe Gly Ala Phe Val Asp Lys Pro	
74	175 180 185	
76	gtg tca cca tac atg tat atc tcc cca cca gag gcc ctc gaa aac ccc	626
77	Val Ser Pro Tyr Met Tyr Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro	
78	190 195 200	
80	tgc tat gat atg aag acc acc tgc ttg ccc atg ttt ggc tac aaa cac	674
81	Cys Tyr Asp Met Lys Thr Thr Cys Leu Pro Met Phe Gly Tyr Lys His	
82	205 210 215	
84	gtg ctg acg cta act gac cag gtg acc cgc ttc aat gag gaa gtg aag	722
85	Val Leu Thr Leu Thr Asp Gln Val Thr Arg Phe Asn Glu Glu Val Lys	
86	220 225 230	
88	aag cag agt gtg tca cgg aac cga gat gcc cca gag ggt ggc ttt gat	770
89	Lys Gln Ser Val Ser Arg Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp	
90	235 240 245 250	
92	gcc atc atg cag gct aca gtc tgt gat gaa aag att ggc tgg agg aat	818
93	Ala Ile Met Gln Ala Thr Val Cys Asp Glu Lys Ile Gly Trp Arg Asn	
94	255 260 265	
96	gat gca tcc cac ttg ctg gtg ttt acc act gat gcc aag act cat ata	866
97	Asp Ala Ser His Leu Leu Val Phe Thr Thr Asp Ala Lys Thr His Ile	
98	270 275 280	
100	gca ttg gac gga agg ctg gca ggc att gtc cag cct aat gac ggg cag	914
101	Ala Leu Asp Gly Arg Leu Ala Gly Ile Val Gln Pro Asn Asp Gly Gln	
102	285 290 295	
104	tgt cat gtt ggt agt gac aat cat tac tct gcc tcc act acc atg gat	962
105	Cys His Val Gly Ser Asp Asn His Tyr Ser Ala Ser Thr Thr Met Asp	
106	300 305 310	
108	tat ccc tct ttg ggg ctg atg act gag aag cta tcc cag aaa aac atc	1010
109	Tyr Pro Ser Leu Gly Leu Met Thr Glu Lys Leu Ser Gln Lys Asn Ile	
110	315 320 325 330	
112	aat ttg atc ttt gca gtg act gaa aat gta gtc aat ctc tat cag aac	1058
113	Asn Leu Ile Phe Ala Val Thr Glu Asn Val Val Asn Leu Tyr Gln Asn	
114	335 340 345	
116	tat agt gag ctc atc cca ggg acc aca gtt ggg gtt ctg tcc atg gat	1106
117	Tyr Ser Glu Leu Ile Pro Gly Thr Thr Val Gly Val Leu Ser Met Asp	
118	350 355 360	
120	tcc agc aat gtc ctc cag ctc att gtt gat gct tat ggg aaa atc cgt	1154
121	Ser Ser Asn Val Leu Gln Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg	
122	365 370 375	
124	tct aaa gtc gag ctg gaa gtg cgt gac ctc cct gaa gag ttg tct cta	1202
125	Ser Lys Val Glu Leu Glu Val Arg Asp Leu Pro Glu Glu Leu Ser Leu	
126	380 385 390	
128	tcc ttc aat gcc acc tgc ctc aac aat gag gtc atc cct ggc ctc aag	1250
129	Ser Phe Asn Ala Thr Cys Leu Asn Asn Glu Val Ile Pro Gly Leu Lys	

## RAW SEQUENCE LISTING

DATE: 01/14/2002

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TIME: 07:44:23

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

130	395	400	405	410	
132	tct tgt atg gga ctc aag att gga gac acg gtg agc ttc agc att gag	1298			
133	Ser Cys Met Gly Leu Lys Ile Gly Asp Thr Val Ser Phe Ser Ile Glu				
134	415 420 425				
136	gcc aag gtg cga ggc tgt ccc cag gag aag gag aag tcc ttt acc ata	1346			
137	Ala Lys Val Arg Gly Cys Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile				
138	430 435 440				
140	aag ccc gtg ggc ttc aag gac agc ctg atc gtc cag gtc acc ttt gat	1394			
141	Lys Pro Val Gly Phe Lys Asp Ser Leu Ile Val Gln Val Thr Phe Asp				
142	445 450 455				
144	tgt gac tgt gcc tgc cag gcc caa gct gaa cct aat agc cat cgc tgc	1442			
145	Cys Asp Cys Ala Cys Gln Ala Gln Ala Glu Pro Asn Ser His Arg Cys				
146	460 465 470				
148	aac aat ggc aat ggg acc ttt gag tgt ggg gta tgc cgt tgt ggg cct	1490			
149	Asn Asn Gly Asn Gly Thr Phe Glu Cys Gly Val Cys Arg Cys Gly Pro				
150	475 480 485 490				
152	ggc tgg ctg gga tcc cag tgt gag tgc tca gag gag gac tat cgc cct	1538			
153	Gly Trp Leu Gly Ser Gln Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro				
154	495 500 505				
156	tcc cag cag gac gag tgc agc ccc cga gag ggt cag ccc gtc tgc agc	1586			
157	Ser Gln Gln Asp Glu Cys Ser Pro Arg Glu Gly Gln Pro Val Cys Ser				
158	510 515 520				
160	cag cgg ggc gag tgc ctc tgt ggt caa tgt gtc tgc cac agc agt gac	1634			
161	Gln Arg Gly Glu Cys Leu Cys Gly Gln Cys Val Cys His Ser Ser Asp				
162	525 530 535				
164	ttt ggc aag atc acg ggc aag tac tgc gag tgt gac gac ttc tcc tgt	1682			
165	Phe Gly Lys Ile Thr Gly Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys				
166	540 545 550				
168	gtc cgc tac aag ggg gag atg tgc tca ggc cat ggc cag tgc agc tgt	1730			
169	Val Arg Tyr Lys Gly Glu Met Cys Ser Gly His Gly Gln Cys Ser Cys				
170	555 560 565 570				
172	ggg gac tgc ctg tgt gac tcc gac tgg acc ggc tac tac tgc aac tgt	1778			
173	Gly Asp Cys Leu Cys Asp Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys				
174	575 580 585				
176	acc acg cgt act gac acc tgc atg tcc agc aat ggg ctg ctg tgc agc	1826			
177	Thr Thr Arg Thr Asp Thr Cys Met Ser Ser Asn Gly Leu Leu Cys Ser				
178	590 595 600				
180	ggc cgc ggc aag tgt gaa tgt ggc agc tgt gtc tgt atc cag ccg ggc	1874			
181	Gly Arg Gly Lys Cys Glu Cys Gly Ser Cys Val Cys Ile Gln Pro Gly				
182	605 610 615				
184	tcc tat ggg gac acc tgt gag aag tgc ccc acc tgc cca gat gcc tgc	1922			
185	Ser Tyr Gly Asp Thr Cys Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys				
186	620 625 630				
188	acc ttt aag aaa gaa tgt gtg gag tgt aag aag ttt gac cgg gag ccc	1970			
189	Thr Phe Lys Lys Glu Cys Val Glu Cys Lys Lys Phe Asp Arg Glu Pro				
190	635 640 645 650				
192	tac atg acc gaa aat acc tgc aac cgt tac tgc cgt gac gag att gag	2018			
193	Tyr Met Thr Glu Asn Thr Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu				
194	655 660 665				

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002

TIME: 07:44:23

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

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196   tca gtg aaa gag ctt aag gac act ggc aag gat gca gtg aat tgt acc      2066
197   Ser Val Lys Glu Leu Lys Asp Thr Gly Lys Asp Ala Val Asn Cys Thr
198               670                      675                      680
200   tat aag aat gag gat gac tgt gtc gtc aga ttc cag tac tat gaa gat      2114
201   Tyr Lys Asn Glu Asp Asp Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp
202               685                      690                      695
204   tct agt gga aag tcc atc ctg tat gtg gta gaa gag cca gag tgt ccc      2162
205   Ser Ser Gly Lys Ser Ile Leu Tyr Val Val Glu Glu Pro Glu Cys Pro
206               700                      705                      710
208   aag ggc cct gac atc ctg gtg gtc ctg ctc tca gtg atg ggg gcc att      2210
209   Lys Gly Pro Asp Ile Leu Val Val Leu Leu Ser Val Met Gly Ala Ile
210               715                      720                      725                      730
212   ctg ctc att ggc ctt gcc gcc ctg ctc atc tgg aaa ctc ctc atc acc      2258
213   Leu Leu Ile Gly Leu Ala Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr
214               735                      740                      745
216   atc cac gac cga aaa gaa ttc gct aaa ttt gag gaa gaa cgc gcc aga      2306
217   Ile His Asp Arg Lys Glu Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg
218               750                      755                      760
220   gca aaa tgg gac aca gcc aac aac cca ctg tat aaa gag gcc acg tct      2354
221   Ala Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser
222               765                      770                      775
224   acc ttc acc aat atc acg tac cgg ggc act taa tgataagcag tcatacctcag      2407
225   Thr Phe Thr Asn Ile Thr Tyr Arg Gly Thr
226               780                      785
228   atcattatca gcctgtgccca ggattgcagg agtcacctgcc atcatgttta cagaggacag      2467
230   tattttgtggg gagggatttc ggggctcaga gtggggtagg ttggggagaat gtcagtatgt      2527
232   ggaagtgtgg gtctgtgtgt gtgtatgtgg ggggtctgtgt gtttatgtgt gtgtgttgtg      2587
234   tgtgggagtg tgtaatttaa aatttgtgatg tgacctgata agctgagctc cttagccttt      2647
236   gtcccagaat gcctcctgca gggattcttc ctgcttagct tgagggtgac tatggagctg      2707
238   agcaggtgtt cttcattacc tcagtgaaga gccagctttc ctcatcaggc cattgtccct      2767
240   gaagagaagg gcagggctga ggcctctcat tccagaggaa gggacaccaa gccttggtc      2827
242   taccctgagt tcataaattt atggttctca ggcctgactc tcagcagcta tggtaggaac      2887
244   tgctggcttg gcagcccggg tcatctgtac ctctgcctcc tttcccctcc ctcaggccga      2947
246   aggaggagtc agggagagct gaactattag agctgcctgt gccttttgcc atcccctcaa      3007
248   cccagctatg gttctctcgc aagggaagtc cttgcaagct aattctttga cctgttgga      3067
250   gtgaggatgt ctgggccact caggggtcat tcatggcctg ggggatgtac cagcatctcc      3127
252   cagttcataa tcacaaccct tcagatttgc cttattggca gcg                      3170

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255 &lt;210&gt; SEQ ID NO: 2

256 &lt;211&gt; LENGTH: 23

257 &lt;212&gt; TYPE: DNA

258 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 260 &lt;220&gt; FEATURE:

260 &lt;223&gt; OTHER INFORMATION: PCR Primer

262 &lt;400&gt; SEQUENCE: 2

263 tttaccactg atgccaagac tca

266 &lt;210&gt; SEQ ID NO: 3

267 &lt;211&gt; LENGTH: 21

268 &lt;212&gt; TYPE: DNA

269 &lt;213&gt; ORGANISM: Artificial Sequence

*insert the mandatory  
number identifier whenever*

23 &lt;2217, &lt;2227,

*or <2237 is  
shown*

*(global error)*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002  
TIME: 07:44:23

Input Set : A:\Sequence  
Output Set: N:\CRF3\01142002\J018445.raw

W--> 271 **<220>** FEATURE: *same error*  
271 <223> OTHER INFORMATION: PCR Primer  
273 <400> SEQUENCE: 3  
274 ccgtcattag gctggacaat g 21  
277 <210> SEQ ID NO: 4  
278 <211> LENGTH: 25  
279 <212> TYPE: DNA  
280 <213> ORGANISM: Artificial Sequence  
W--> 282 **<220>** FEATURE:  
282 <223> OTHER INFORMATION: PCR Probe  
284 <400> SEQUENCE: 4 25  
285 atagcattgg acggaaggct ggcag  
288 <210> SEQ ID NO: 5  
289 <211> LENGTH: 19  
290 <212> TYPE: DNA  
291 <213> ORGANISM: Artificial Sequence  
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293 <223> OTHER INFORMATION: PCR Primer  
295 <400> SEQUENCE: 5 19  
296 gaaggtgaag gtcggagtc  
299 <210> SEQ ID NO: 6  
300 <211> LENGTH: 20  
301 <212> TYPE: DNA  
302 <213> ORGANISM: Artificial Sequence  
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304 <223> OTHER INFORMATION: PCR Primer  
306 <400> SEQUENCE: 6 20  
307 gaagatggtg atgggatttc  
310 <210> SEQ ID NO: 7  
311 <211> LENGTH: 20  
312 <212> TYPE: DNA  
313 <213> ORGANISM: Artificial Sequence  
W--> 315 **<220>** FEATURE:  
315 <223> OTHER INFORMATION: PCR Probe  
317 <400> SEQUENCE: 7 20  
318 caagcttccc gttctcagcc  
321 <210> SEQ ID NO: 8  
322 <211> LENGTH: 18  
323 <212> TYPE: DNA  
324 <213> ORGANISM: Artificial Sequence  
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326 <223> OTHER INFORMATION: Antisense Oligonucleotide  
328 <400> SEQUENCE: 8 18  
329 gcatctcgtc cgctctccc  
332 <210> SEQ ID NO: 9  
333 <211> LENGTH: 18  
334 <212> TYPE: DNA  
335 <213> ORGANISM: Artificial Sequence  
W--> 337 **<220>** FEATURE:

The types of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002

TIME: 07:44:24

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:58 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:260 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:271 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:282 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:293 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:304 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:315 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:326 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:337 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:348 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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L:370 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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L:414 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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L:436 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:447 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:458 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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L:579 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:590 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:601 M:258 W: Mandatory Feature missing, <220> FEATURE:  
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/018,445

DATE: 01/14/2002

TIME: 07:44:24

Input Set : A:\Sequence

Output Set: N:\CRF3\01142002\J018445.raw

L:755 M:258 W: Mandatory Feature missing, <220> FEATURE: